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AC006917 Genomic s
Y11337 A.thali-
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Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; endicotyledons; core endicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
I (bases I to 1964)
Harberd, N. P., Peng, J., Carol, P. and Richards, D. E.
NUCLEIC ACID ENCODING GAI GENE OF ARABIDOPSIS THALIANA
Patent: WO 9729123-A 1 14 AUG-1997;
INNES JOHN CENTRE INNOV LTD (GB)
Other publication AU 1799697 19970828.
                                                                              A64701 Sequence 5
A64701 Sequence 9
AR174881 Sequence
A64703 Sequence 7
AR174882 Sequence 7
Y1135 A. thaliana
AY052239 Arabidops
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AX081276 Sequence
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AYO70035 Arabidops
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/strain="LANDSBERG ERECTA"
/db_xref="taxon:3702"
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                                                                     May 11, 2002, 14:49:19 ; Search time 1945.53 Seconds
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       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Listing first 45 summaries
                                             nucleic search, using sw model
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| DEFINITION Sequence 1 from patent US 6307126. ACCESSION VERSION VERSION AR174879.1 GI:17915199 SOURCE ORGANISM Unknown. Unclassified. AUTHORS Harberd, N.P., Peng, J., Richards, D.E. and Carol, P. AUTHORS TITLE Nucleic acid encoding GAI gene of Arabidopsis thaliana JOURNAL FEATURES 1 Location/Qualifiers SOURCE AUTHOR AUTHORS TITLE JOURNAL FEATURES 1 Location/Qualifiers SOURCE JOURNAL FATORE AUTHOR | Query Match Query Match Best Local Similarity 100.0%; Score 1964; DB 6; Length 1964; Matches 1964; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 taataatcatttttttcttataaccttcctctatttttacaatttatttgttatta 60 |

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Peng, J., Carol, P., Richards, D.E., King, K.E., Cowling, R.J., Murphy, G.P. and Harberd, N.P.
The Arabidopsis GAI gene defines a signalling pathway that negatively regulates gibberellin responses
Genes Dev. In press
2 (bases I to 1964)
Harberd, N.P.
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Submitted (22-OCT-1997) N.P. Harberd, John J
Genetics, Colney Lane, Norwich, NR4 70J, UK
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             661 GTCAACTCGGCATGTTGTCCTGGTTGACTCGCAGGAGAACGGTGTGCGTCTCGTTCACGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cttcgccgaagctctcgcggcggatttaccgtctctctccgtcgcagagtccaatcga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ccactctctctccgatactcttcagatgcacttctacgagacttgtccttatctcaagtt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              961 CGCTCACTTCACGGCGAATCAAGCGATTCTCGAAGCTTTTCAAGGGAAGAAAAGAGTTCA
                      121 AGATTCTTCACCTTCCCAAATAAAGCAAAACCTAGATCCGACATTGAAGGAAAAACCTTT
                                                tagatccatctctgaaaaaaaaccaaccatgaagagagatcatcatcatcatcaaga
                                                                                                                                                                                                                                           tgttcactataatccggcggagctttacacgtggcttgattctatgctcaccgaccttaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δ
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join(26661. .26948,27454. .27610,27713. .27814,27911. .28038,28342. .28470,28565. .28632,28747. .28969)
/note="similar to acid phosphatase type 5 emb|CAB63938.1; similar to EST gb|N96048.1"
                                                                                                                                                                                                                                                                                                                                                                 SLKEKLAAVRPMLEDLRLQKDERMKQFVDIKAQIEKMSGEISGYSDQLNKTWVGSLAL
DEQDLTLRKLNEYQTHLRSLQKEKSDRLNKVLDYVNEVHTLGGVLGVDFGQTYSEVHP
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IVRPYEVKSLGESFKSLCSPKEGSKVIFGQALKVGTSLTFVGEAVRDKAGNLMIQKSK
EQSLIVFSEESSFDEMVNNMKSQSELCVILAKIFGSIAVAIAVVYGVDYARKVLLPFV
                                                                     complement(join(20071, __20409,20499, _20573,20648, _20721, 20800, _20687,20957, _21108,21188, _21356,21448, _21906, _22006, _22275,22367, _22570,22840, _22917))
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ELEKECLEIYRRKVDEAANSKAQLHQSLVSIEAEIASLLAALGVFNSHSPMKAKEGSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KRLVDPSELLTNIELHINKIKEEAHSRKEIIDRIDRWLSACEEENWLEEYNQDETRYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KLTRKQQEEEKRRYRDQKKMQDLLIKRRESIYGSKPSPRRSNSVRKTNGYNGDASVPP
TPRRNSAGATNNDIMTTPRSYSSHRQNGYFKEVRRLSTAPLNFVAIPKEDSVSTYTSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGRGGHVNLKHAERARITVNKIPSMVDNLIKKTLLWEDETRKSFLYDGVRLVSILEDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Db 117187 TAATAATCATTTTTTTTTTTTTACCTTCCTCTCTATTTTTACAATTTATTTGTTATTA 117246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gaagtggtagtggagtgaaaaaaaaacaaatcctaagcagtcctaaccgatccccgaagctaa 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       taatcctccgtcgtctaacgccgagtacgatcttaaagctattcccggtgacgcgattct 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 taataatcatttttttttttttataaccttcctctctatttttacaatttattttgttatta 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        111307 AGATTCTTCACCTTCCCAAATAAAGCAAAACCTAGATCCGACATTGAAGGAAAAACCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            agataagaagactatgatgatgaatgaagaagacgacggtaacggcatggatgagcttct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  agattetteacetteecaaataaageaaaacetagateegacattgaaggaaaaaeettt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGATAAGAAGACTATGATGATGAAGAAGACGACGGTAACGGCATGGATGAGCTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gactgttcactataatccggcggagctttacacgtggcttgattctatgctcaccgacct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tagatccatctctgaaaaaaaaccaaccatgaagagag----atcatcatcatcatca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACTGTTCACTATAATCCGGGGGAGCTTTACACGTGGCTTGATTCTATGCTCACCGACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 132699,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 8;
                                                    WKKKDLGDSSSQNGSSDSEDTDISDF"
                                                                                                                                                                                                         /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1922.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 0;
                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CGSEPDSPLYN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 97.9%;
Best Local Similarity 99.2%;
Matches 1943; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Marc.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117487
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                                                                             CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                q
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                                                                                                                                                                              VRNLLLTGCLFCGPLFLTFCFLNTVAITYTATAALPFGTIVVIVLIMTLVTSPLLVLG
GIAGKNSKAEFQAPCRTTKYPREIPPLPWYRSAIPQMAMAGFLPFSAIYIELYYIFAS
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ASFVSKDESISLGRIFLEANSEEDKCCETLLRKWDQLKPTTQKFVSLVSMVKRIEKEK
FLYHQDRESLAREDEVELVSEQNRELDRENKFLRQCSAERSHGSNKFNKRKSIKMMSSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MKLWKRAAVVLKDGPSLIAADDILTAAVVKATSHDELSIDTESA
QFIYRHVLSSPSSLKPLVSLISSRVKRTRSWAVALKGLMLMHGFFLCKSTVAESIGRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IIRKMQIIVDSLIRIKPIGENMMIPVINEAMENVVSEIMEIYGWICRRIAEVLPNVHS
KIGKTEADLALKIVAKSMKOGGELKKYFEFCKDLGVSNAQEIPNFVRIPEADVIHLDE
LVRTAMESSEESAERTEIAEEEEEEEEETTKLSDLITLDHNEEAPASPPRVVVUIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MEFKÁYPILYWFQPFRLQCEPVIVLFLCFQMICLKKKQRIFLFW
YPEELHLQQPLTPKMVIFWVLFLRIRWWFDKQVCKSSSTTKGDSLVSVGAEGALGFNE
                                                                                                                                                     TQLFTLTIFIFMLALVGVFYPYNRGALFTALVVIYALTSGIAGYTSASFYCQLEGKSW
                                                                                                                                                                                                                                                                YAYCLYYYYARSDMSGFMQTSFFFGYMACICYGFFLMLGTVGFRAALLFVRHIYRSIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RSYHRRIDVISSPQINHTRFPFTSLRRVKQLARLKWKTAEERNEEEEDDTEETSTEEK
MTVQRRRKSKFTAEQREAMKDYAAKLGWTLKDKRALREEIRVFCEGIGVTRYHFKTWV
                                                                                                                               /translation="MLKRYAQDEEAADDQEETGWKYIHGDVFRFPTHNSLFAASLGSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PFDLSSFGEGNSRIMSKSGGFNLFVRAYFAFLDRRSILFHDGNRHRYNEESSVLIRLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MQSTCVYRECMRNHAAKLGSYAIDGCREYSQPSTGDLCVACGCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(join(17635, .17815,17901, .18019,18141, .18194,
18300, .18406,18547, .18611,18742, .18950))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="unknown protein; similar to EST gb|AI995472.1"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                           /note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(13762. .14781)
/note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16027. .16533/note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                       /evidence=not_experimental/product="F10B6.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /evidence=not_experimental/product="F10B6.8"
                        /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence=not_experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAF79220.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAF79249.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IEKRIELSSQEFID"
11067. .11906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="F10B6.
                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                               .9714
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| .26 | 98, | 146 | 900 | • 991 | 126 | 986 | .46 | 90: | 99; | | 98 | 46 | 90 | 99 | 26 | 98 | 46 | |
|--------|--|--|--|--|---|---|---|--|---|---|--|---|--|---|--|--|--|--|
| 1177 | 597 1177 | 657 1178 | 717 1179 | 777 1179 | 837 1180 | 897 1180 | 957 1181 | 1017 | 1077 1182 | 1137 1183 | 1197 1183 | 1257 1184 | 1317 | 1377 | 1437 | 1497 1186 | 1557 1187 | 1617 |
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| qq | Qy | Qy Db | Oy Db | Qy Db | Qy Db | Qy Db | Oy Dp | Oy Dp | Oy Dp | Qy Db | Qy Db | Qy Db | Oy Db | Qy Db | Qy Db | Oy Dp | Qy Db | Οy |

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Truong, H. N., Caboche, M. and Daniel-Vedele, F.
Sequence and characterization of two Arabidopsis thaliana cDNAs isolated by functional complementation of a yeast gln3 gdh1 mutant FEBS Lett. 410 (2-3), 213-218 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (13-FEB-1997) H.N. Truong, INRA-Versailles, Laboratoire
de Biologie Cellulaire, Route de Saint-Cyr, 78026 Versailles Cedex,
FRANCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                    Db 119047 CGACCGAAGCCAAACTAAATCCTACTTTTTTCCCTTTGTCACTTGTTAAGATCTTATCT 119106
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Y11337.1 GI:2339979.
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Truong, H.N.
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| 7 May 1 May | Db 914 TGCACTTCTACGAGACTTGTCCTTATCTCAAGTTCGCTCACTTCACGGCGAATCAAGCGA 973 Qy 987 ttctcgaagcttttcaagggaagaaagagttcatgtcattgatttctctatgagtcaag 104 Db 974 TTCTCGAAGCTTTCAAGGGAAGAAAAGAGTTCATGTCATTGATTTCTCTATGAGTCAAG 103 | Oy 1047 glottcaatggccggcgcttatgcaggctcttgcgcttcgacctggtggtcctcctgtt 1106 1014 111111111111111111111111111111 | Oy 1107 tocggttaaccggaattggtccaccggcaccggataatttcgattatcttcatgaagttg 1166 | Qy 1167 ggtgtaagctggctcatttagctgaggcgattcacgttgagtttgagtacagagatttg 1226 | Oy 1227 tggctaacactttagctgatcttgatgcttcgatgctttgagcttagaccaagtgagattg 1286 | Oy 1287 aatctgttgcggttaactctgttttcgagcttcacaagctcttgggacgacctggtgcga 1346 | Oy 1347 tcgataaggttcttggtgtggtgaatcagattaaaccggagattttcactgtggttgagc 1406 | Oy 1407 aggaatcgaaccataatagtccgattttcttagatcggtttactgagtcgttgcattatt 1466 | Oy 1467 actogacgttgtttgactcgttggaaggtgtaccgagtggtcaagacaaggtcatgtcgg 1526 | Oy 1527 aggtttacttgggtaaacagatctgcaacgttgtggcttgtgatggacctgaccgattg 1586 | Oy 1587 agcgtcatgaaacgttgagtcagtggaggaaccggttcggggtctgctgggtttgcggctg 1646 | Qy 1647 cacatattggttcgaatgcgtttaagcaagcgagtatgctttggctctgttcaacggcg 1706 | Oy 1707 gtgagggttatcgggtggaggaggtgacggctgtctcatgttgggttggcacacacgac 1766 | Oy 1767 cgctcatagccacctcggcttggaaactctccaccaattagatggtgctcaatgaattg 1826 | Qy 1827 atctgttgaaccggttatgatgatagatttccgaccgaagccaaactaaatcctactgtt 1886 | Oy 1887 tttccctttgtcacttgttaagatcttatctttcattattaggtaattgaaaatttc 1946 | Oy 1947 taaattactcacact 1961 Db 1934 AATCTCGCCTAAATT 1948 |
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| ORIGIN Makest Coner, Co | NSVFELHKLLGRPGAIDKVLGVVNQIKP LFDSLEGVPSGODKVMSEVYLGKQICNV HIGSNAFKQASMLLALFNGGEGYRVEES | в 8; Length 1951; 17: Indels 0; Gaps 0; | aaacaa 86 | taaagc 1 | aaccaa 20 | 26 | ggtcat 32, | atgttc 38 | agcttt 44 | gtacg 50 | ttctt 56 | geteaa 62 | Eggttg 68 | statte 74 | ctgttt 80 | 39cgga 86 | tcaga 92 |

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Cheuk,R., Chen,H., Kim,C.J., Koesema,E., Meyers,M.C., Banh,J.,
Bowser,L., Carninci,P., Dale,J.M., Goldsmith,A.D., Hayashizaki,Y.,
Ishida,J., Jiang,P.X., Jones,T., Kamiya,A., Karlin-Neumann,G.,
Narusaka,M., Nguyen,M., Onoes,T., Palm.,S.X., Miranda,M.,
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Arabidopsis cDNA clones
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Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J.,
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Toriuni, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K.,
Davis, R.W., Theologis, A. and Ecker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL CDNAS: Chen, K., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Shinn, P., Banh, J. Bowser, L., Lan, C.J., Goldsmith, A.D., Jiang, P. X., Jones, T., Karlin Neumann, G., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Nguyen, M., Ondera, C.S., Palm, P.K., Quach, H.L., Southwick, A., Tang, C.C., Toriuni, M., Yamada, K., Yamamnra, Y., Yu, G., Yu, S., Davis, R.W., Theologis, A., and Ecker, J.R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAS (RAFL cDNA : 'RIKEN ATABLÉGOSIS Full-Length cDNA') : Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (28-AUG-2001) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
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                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
      Arubaly4 2097 bp mRNA linear PLN 04-
Arabidopsis thaliana At1g14920/F10B6_15 mRNA, complete cds.
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PEI FTVVEQDSINHOS IFLDRFTESLHYY STLFDSLEGVPSGDDKWSEYY LGKQICK
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                                                       Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 1643)
Harberd, N.P., Peng, J., Carol, P. and Richards, D.E.
WUCLEIC ACID ENCOING GAI GENE OF ARABIDOPSIS THALIANA
Patent: WO 9729123-A 3 14-AUG-1997;
INNES JOHN CENTRE INNOV LTD (GB)
Other publication AU 1799697 19970828.
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Harberd, N.P., Peng, J., Richards, D.E. and Carol, P.
Nucleic acid encoding GAI gene of Arabidopsis thaliana
Patent: US 6307126-A 3 23-OCT-2001;
Location/Qualifiers
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| rocus | TION ION N DS | SOURCE tha ORGANISM Aral Euk | | NAL T ES | Ö | /map="10" /map=" | ORIGIN. Query Match | Best Local Similarity Matches 1642; Conserv Qy 59 tagaagtggtagt; | Db 1 TAGAAGTGGTAGTGGAGTGAAAAACAAA | Db 61 AAGATTCTTCACCTTCCCAAATAAGCA | Db 121 TTAGATCCATCTCTGAAAAAAACCAAC Qy 239 gataagaagactatgatgatgaatgaaga | Db 181 GATAAGAAGACTATGATGATGAATGAAGAAGA Qy 299 gctgttcttggttacaaggttaggtcatc | Db 229 | Db 250 CAGCTTGAAGTTATGATGTCTAATGTTCA Oy 419 actgttcactataatccggcggagcttta | Db 310 ACTGTTCACTATATCCGGGGGGGGGGGGGGGGGGGGGGG | Db 370 AATCCTCGGTCTAACGCCGAGTACGA | | Qy 599 actacaaacaagcggttgaaatgctcaaa |
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| 610 GCGCTTTTGGCTTGCGCTGAAGCTGTTCAGAAGGAGAATCTGACTGTGGCGGAAGCTCTG 669 | 779 gtgaagcaaatcggattcttagctgtttctcaaatcggagctatgagaaaagtcgctact 8 | 839 tacttogcogaagctotogoggoggatttacogtotototocgtogoagagtocaate 898 | 899 gaccactctctccgatactcttcagatgcacttctacgagacttgtccttatctcaag 958 | 959 ttcgctcacttcacggcgaatcaagcgattctcgaagcttttcaagggaagaagaagtt 1018 | 1019 catgtcattgatttctctatgagtcaaggtcttcaatggccggcgcttatgcaggctctt 1078 | 1079 gegettegacetggtgeteetetgtttteeggttaaceggaattggteeacegggaeeg 1138 | 1139 gataatttogattatottoatgaagttgggtgtaagotggctoatttagotgaggogatt 1198 | 1199 cacgttgagtttgagtacagaggatttgtggctaacactttagctgatcttgatgcttcg 1258 | 1259 atgettgagettagaccaagtgagattgaatetgttgeggttaaetetgtttegagett 1318 | 1319 cacaagctcttgggacgacctggtgcgatcgataaggttcttggtgtggtgaatcagatt 1378 | 1379 aaaccggagatttcactgtggttgagcaggaatcgaaccataatagtccgattttctta 1438 | 1439 gatcggtttactgagtcgttgcattattactcgacgttgtttgactcgttggaaggtgta 1498 | 1499 ccgagtgtcaagacaaggtcatgtcggaggtttacttgggtaaacagatctgcaacgtt 1558 | 1559 gtggcttgtgatggacctgaccgagttgagcgtcatgaaacgttgagtcagtggaggaac 1618 | 1619 cggttcgggtttgcgggttgcggctgcacatattggttcgaatgcgtttaagcaagc | 1679 agtatgettttggetetgtteaaeggeggtgaggttategggtggaggagagtgaegge 1738 | 1739 tgtctcatgttggg 1 | 1630 rererentinge |
| d d | Oy Db | Oy Op | Oy Dp | Qy Db | oy Op | yo da ' | 6 6 | Qy Db | Oy Dp | Oy Db | Qy Db | Oy Db | Oy Db | Qy Db | Q Dp | δλ QΩ | δλ | qΩ |

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RESULT A64701

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PAT 29-MAR-1999
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                                                      Streptophyta; Embryophyta; Tracheophyta;
rta; eudicotyledons; core eudicots;
stcales; Brassicaceae; Arabidopsis.
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I GENE OF ARABIDOPSIS THALIANA
4-AUG-1997;
LID (GB)
19697 19970828.
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                                                                                                                                                                                                                             DB 6; Length 1642;
linear
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NG ERECTA"
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DNA
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d. No. 0;
Mismatches
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| Db 1629 TGTCTCATGTTGGG 1642 | RESULT 10 A64705 LOCUS A64705 DEFINITION Sequence 9 from Patent W09729123. | A64705 A64705.1 GI:4530766 | SOURCE thale cress. ORGANISM Arabidopsis thaliana ORGANISM; Varidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; | KOSIGAE; GUTOSIGS 11; BTASSICALES; BTASSICACEAE; ATADIGOPSI 1 (bases 1 to 1642) Harberd, N. P., Peng, J., Carol, P. and Richards, D. E. NUCLEIC ACID ENCODING GAI GENE OF ARABIDOPSIS THALIANA | | <pre>source 11642 /organism="Arabidopsis thaliana" /strain="LaNOSBERG ERECTA" /db_xref="taxon:3702"</pre> | /chromosome="1" /map="20.9" /haplotype="GAI-D7" BASE COUNT 405 a 360 c 423 g 454 t | Match | Best Local Similarity 96.9%; Pred. No. 0; Matches 1642; Conservative 0; Mismatches 0; Indels 52; Gaps 2; Qy 59 taqaaqtqqtaqtqqaqtqaaaaaacaaatcctaaqcaqtcctaaccqaaqct 118 | | Qy 119 aaagattetteacetteecaataaageaaaacetagateegacattgaaggaaaaace 178 | 179 tttagatccatctctgaaaaaaaccaaccatgaagagagatcatcatcatcatcatcaa | Db 121 TTTAGATCCATCTCTGAAAAAAACCAACCATGAAGAGAGATCATCATCATCATCATCATTA 180 Qy 239 gataagaagactatgatgatgaagaagaagaagaagaagaagaagaagaag | Db 181 GATAAGAACTATGATGAATGAAGACGACGCAAGCACGCATG 228 Qy 299 gctgttcttggttacaaggttaggtcatcggaaatggctgatgttgctcagaaactcgag 358 | 229GATGTTGCTCAGAAACTCGAG | Oy 359 cagcttgaagttatgatgtctaatgttcaagaagacgatctttctcaactcgctactgag 418 IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII | 419 actgttcactataatccggggggctttacacgttggcttcattctcaccgcctt | 310 ACTGITCACTATAATCCGGGGGGGCTTTACACGGTGGCTTGATCTATGCTCACCGACCT 36 | 4/9 adrectedgregregatesgagatesgarettaaagteagatese 538 | Oy 539 aatcagttcgctatcgattcggcttcttcgtctaaccaaggcggcggaggagatacgtat 598 | Db 430 AATCAGTTCGCTATCGATTCGGCTTCTTCGTCTAACCAAGCGGCGGCGGAGATACGTA 489 |
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| | 9 gcgettttggattgcgctgaagctgttc | Oy 779 gtgaagcaaatcggattcttagctgtttctcaaatcggagctatgaaaagtcgctact 838 | Qy 839 tacttcgccgaagctctcgcgcggcggatttaccgtctctccgtcgcagagtccaatc 898 | Oy 899 gaccactctctcccgatactcttcagatgcacttctacgagacttgtccttatctcaag 958 | QY 959 ttcgctcacttcacggcgatcaagcgattctcgaagcgtttcaagggaagaagagtt 1018 | Qy 1019 catgicattgatttctctatgagtcaaggtcttcaatggccggcgcttatgcaggctct 1078 | QY 1079 gcgcttcgacctggtggtctcctgttttccggttaaccggaattggtccaccggcaccg 1138 | Oy 1139 gataattcgattatcttcatgaagttgggtgtaagctggctcatttagctgaggcgatt 1198 | Oy 1199 cacgttgagtttgagtacagaggatttgtggctaacatttagctgatcttgatgcttcg 1258 | 1259 atgettgagettagaccaagtgagattgaatetgttgeggttaaetetgtttegagett | VGAGCTTAGACCAAGTGAGATTGAATCTGTTGCGGGTTAACTCTGTTTTC | 1209 CACAAGCTCTTGGGACGACCTGGTGCGATCGATAAGGTTCTTGGTGTGGTGAATCAGATT | <pre>QY 1379 aaaccggagatttcactgtggttgagcaggaatcgaaccataatagtccgattttctta 1438</pre> | Oy 1439 gatcggtttactgagtcgttgcattattactcgacgttgtttgactcgttggaaggtgta 1498 | 1499 ccgagtggtcaagacaaggtcatgtcggaggtttacttgggtaaacagatctgcaacgtt | AGT qct | 1449 GTGGCTTGTGATGGACCTGACCGAGTTGAGCGTCATGAAACGTTGAGTGGAGGAAC | ٦, | 1679 agtatgettttggetetgtteaaeggeggtgagggttategggtggaggagagt | Db 1569 AGTATGCTTTTGGCTCTGTTCAACGGCGGTGAGGGTTATCGGGTGGAGGAGGTGACGGC 1628 | Qy 1739 tgtctcatgttggg 1752 |

| Qy Dp | 599 | actacaaacaagggttgaaatgctcaaaggggtcgtggaaaccacaagggacggct 658 | 15 |
|----------|------|--|---------------------------------------|
| Qy Db | 659 | gagtcaactcggcatgttgtcctggttgactcgcaggagaacggtgtgcgtctcgttcac 718 | Qy 173 Db 162 |
| oy O | 719 | gcgctttggcttgcg | RESULT AR174881 LOCUS |
| oy Op | 977 | gtgaagcaaatoggattottagotgtttotcaaatoggagotatgagaaaagtogotaot 838 | DEFINITION ACCESSION VERSION KEYWORDS |
| Qy | 839 | tacttogcogaagctotogogoggatttacogtotototocgtogoagagtocaato 898 | SOURCE ORGANI: REFERENCI |
| Oy Dp | 899 | gaccactctctccgatactcttcagatgcacttctacgagacttgtccttatctcaag 958 | |
| Oy Op | 959 | ttcgctcacttcacggcgaatcaagcgattctcgaagcttttcaagggaagaagagtt 1018 | SOUT BASE COUT ORIGIN |
| Qy Dp | 1019 | catgicattgattictctatgagicaaggicttcaatggccggcgcttatgcaggctctt 1078 | Query Best L |
| Qy Db | 1079 | gogottogacotggtoctoctgttttocggttaacoggaattggtocacoggcacog 1138 | ia cone |
| Qy Dp | 1139 | gataatttogattatottoatgaagttgggtgtaagotggotoatttagotgagogatt 1198 | Db Qy 119 |
| Oy Db | 1199 | | Db 6. |
| oy O | 1259 | atgettgagettagaccaagtgagattgaatetgttgeggttaaetetgtttegagett 131 | Db 12: Qy 239 |
| Oy Dp | 1319 | cacaagetettgggacgacetggtgcgateggttettggtgtggtg | Db 18: Qy 299 |
| Oy Op | 1379 | aaaccggagattttcactgtggttgggcaggaatcgaaccataatagtccgattttctta 143 | 3 8 |
| oy Op | 1439 | <pre>gatcggtttactgattgcattattactcgacgttgtttgactcgtl </pre> | |
| Qy | 1499 | ccgagtggtcaagaccaaggtcatgtcggaggtttacttgggtaaacagatctgcaacgtt 1558 | |
| Oy Dp | 1559 | gtggcttgtgatggacctgaccgagttgagcgtcatgaaacgttgagtcagtggaggaac 1618 | י או הי |
| Qy Db | 1619 | cggttcgggtctgctgggtttgcggctgcacatattggttcgaatgcgtttaagcaagc | 4 10 |
| ٥٥ . | 1679 | agtatgettttggetetgtteaacggcggtgagggttatcgggtggagg | Db 49 |

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                                                                                                                                    1 (bases 1 to 1642)
Harberd, N.P., Peng, J., Richards, D.E. and Carol, P.
Nucleic acid encoding GAI gene of Arabidopsis thaliana
Patent: US 6307126-A 5 23-0CT-2001;
Location/Qualifiers
1. 1642
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96.9%; Pred. No. 0;
iive 0; Mismatches
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|TGTCTCATGTTGGG 1642
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| Db 1629 TGTCTCATGTTGGG 1642 | AR174883 1642 bp | CCESSI CCESSI ERSION EYWORD | Unknown. I Unknown. Unclassified. 1 (bases 1 to 1642) | OMZE | SOURCE 11042 /organism="unknown" BASE COUNT 405 a 360 c 423 g 454 ORIGIN | atch 79.9%; Score 1570; all Similarity 96.9%; Pred. No. 0 | matches 1042; Conservative U; Mu 59 tagaagtggtagtggagtgaaaaaacaaa | 1119 | 179 | 121 TTTAGAT 239 gataaga | 299 | N 60 (| 419 | 479 | 370 AATCCTCCGTCTAACGCCGAGTACGA 539 aatcagttcgctatcgattcggcttcttcc | 430 AATCAGTICGCTATTCGCTTCTTT 599 actacaaacaagcggttgaaatgctcaaa | 490 ACTACAAACAGGGGTTGAAATGCTCAAAACGGG 659 gagtcaaatcggcatgttgtcctggttgaactcg | Db 550 GAGTCAACTCGGCATG-TGTCCTGGTTGACTCGCAG |
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| 659 gagtcaactcggcatgttgtcctggttgactcgcaggagaacggtgtgcgtctcgttcac 718 | 719 gcgcttttggcttgcqctgaagctgttcagaaggagaatctgactgtggcggaagctctg 778 | 779 gtgaagcaaatcggattcttagctgtttctcaaatcggagctatgagaaaagtcgctact 838 | 839 tacttcgccgaagctctcgcgcggatttaccgtctctctc | 899 gaccactctctccgatactcttcagatgcacttctacgagacttgtccttatctcaag 958 | 959 ttcgctcacttcacggcgaatcaagcgattctcgaagcttttcaagggaagaagaggt 1018 | 1019 catgrattgatttctctatgagtcaaggtcttcaatggccggcgcttatgcaggctctt 1078 | 1079 gcgcttcgacctggtggtcctcctgttttccggttaaccggaattggtccaccggcaccg 1138 | 1139 gataatttogattatottoatgaagttgggtgtaagottggctcatttagottgaggcgatt 1198 | 1199 cacgttgagtttgagtacagagatttgtggctaacactttagctgatcttgatgcttcg 1258 | 1259 atgottgagottagaccaagtgagattgaatotgttgcggttaactotgttttcgagott 1318 | 1319 cacaagctcttgggacgacctggtgcgatcgataaggttcttggtgtggtgatcagatt 1378 | 1379 aaaccggagatttcactgfggttgagcaggaatcgaaccataatagtccgattttctta 1438 | 1439 gatcggtttactgagtcgttgcattattactcgacgttgtttgactcgttggaaggtgta 1498 | 1499 ccgagtgftcaagaccatgtcgtggggtttacttgggtaaacagatctgcaacgt 1558 | 1559 gtggtttgtgatggacctgaccgagttgagcgtcatgaacgttgagtcagtggaggaac 1618 | 1619 cggttcgggtctgctgggttgcggctgcacatattggttcgaatgcgtttaagcaagc | 1679 agtatgcttttggctctgttcaacggcggtgaggttatcgggtggagagaga | 1739 tgtctcatgttggg 1752 |
| Qy Db | Qy Db | Qy Dp | Q P P | Qy Dp | oy da | Qy Dp | oy GD | Oy Dp | QQ QD | Qy Db | oy Oy | QY Dp | Oy Db | Qy Db | Oy Dp | Q. Db | Qy Db | Οy |

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hes 0; Indels 52; Gaps
                                      D.E. and Carol, P. f Arabidopsis thaliana 01;
                                                                                 DB 6; Length 1642;
linear
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| T 13 A64703 ITTON Sequence 7 from Patent W09729123. SION A64703.1 GI:4530765 RDS thale cress. Entry Arabidopsis thallana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trache | Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosida II; Brassicales; Brassicaceae; Arabidopsis. Rosidae; Lo 1656) AUTHORS Harberd, N. P., Peng, J., Carol, P. and Richards, D. E. TITLE NUCLEIC ACID ENCODING GAI GENE OF ARABIDOPSIS THALIANA JOURNAL PATENTE INNOV LTD (GB) INNES JOHN CENTRE INNOV LTD (GB) COMMENT Other publication AU 1799697 19970828. | urce UNT 403 a | Query Match Best Local Similarity 96.5%; Score 1556.4; DB 6; Length 1636; Bast Local Similarity 96.5%; Pred. No. 0; Matches 1635; Conservative 0; Mismatches 1; Indels 58; Gaps 2; 59 tagaagigtagagigaaaaaaaaaaaaaaaaaaaaaaa | 1 TAGAAGTGGTAGTGGAAAAAACAAATCCTAAGCAGTCCTAACCGATCCCCGAAGCT 60 119 aaagattcttcaccttcccaaataaagcaaaacctagatccgacattgaaggaaaaacct 178 1119 aaagattctTCACCTTCCCAAATAAAGCAAAACCTAGATCCGACATTGAAGGAAAAACCT 120 179 tttagatccatctctgaaaaaaaaccaaccatgaagagagatcatcatcatcatcatcaa 238 | | cagcttgaagttatgatgtctaatgttcaagaagacgatcttctcaactcgctactgag 41 | 479 aatcctccgtcgtctaacgccgagtacgatcttaaagctattcccggtgacgcgattctc 538 |
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                                                                                                     1 (bases 1 to 1636)
Harberd, N.P., Peng, J., Richards, D.E. and Carol, P.
Nucleic acid encoding GAI gene of Arabidopsis thaliana
Patent: US 6307126-A 7 23-OCT-2001;
Location/Qualifiers
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                                                linear
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PLN 19-AUG-1997
                                                                                                              Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases I to 2210, M. and Daniel-Vedele, F. Sequence and characterization of two Arabidopsis thaliana CDNAs isolated by functional complementation of a yeast gln3 gdh1 mutant 973910
                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (13-FEB-1997) H.N. Truong, INRA-Versailles, Laboratoire
de Biologie Ceilulaire, Route de Saint-Cyr, 78026 Versailles Cedex,
FRANCE
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1. 2210
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/sub_species"(L). Heynh"
/db_xref="taxon:3702" tage seedlings"
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/note="Landsberg erecta ecotype"
132. 1895
/gene="RGA1"
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/protein_id="CAA72177.1"
/db_xref="G1:2339978"
/db_xref="SPTREMBL:023642"
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                    A.thaliana mRNA for RGAl gene.
Y11336
Y11336.1 GI:2339977
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Truong, H.N.
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| οy | 472 | * | |
| q | 446 | AGCTTAATCCTCCTCCTCTTCCGGCGAGTTCTAACGGTTTAGATCCGGTTCTTCCTTC | |
| λa | 498 | cgagtacgatcttaaag | |
| q | 206 | TCCGGCTTCGGATTATGACCTTAAAGTCATTCCCGGAAACGC 56 | |
| S G | 532 | accaaggcggc 5 IIII TCAGAACAAGCGTTT 6 | |
| λα | 84 | oaaacaagcggttgaaatgctcaaacggcgtcgtgga 63 | |
| g G | 26 | rgctcgagtcctgattctatggttacatcgacttcgacgggtacgcagattgg 68 | |
| δλ Op | 640 | TAGGAACGA | |
| λς Gp | 664 | tgactcgcaggagaacggtgtgcgtctcgttcacgcgct 72 | |
| ž t | 724 | ttcagaaggagaatctgactgtggcggaagctctggtgaa 78 | |
| g , | 5 (| AIGGCITGIGCAGAAGCAATCCAGCAGAACAATTTGACTCTAGCGGAAGCTCTTGIGAA 80 | |
| o d | 784 866 | gcaaatoggattottagotgtttotcaaatoggagotatgagaaaagtogotaottaott 843 | |
| Qy Dp | 926 | | |
| λο qα | 904 | tcttcagatgcacttctacgagacttgtccttatctcaagttcgc 963 | |
| δŏ | | | |
| e G | 1046 | CACTICACGGGGAACCAAGCGATTCTCGAAGCTTTTGAAGGTAAGAAGAGGTACACGT 110 | |
| oy Ob | 1024 | cttcaatggccggcgttatgcaggctttgcgct 1 | |
| Oy Ob | 1084 | gaattggtccaccggcaccggataa 114 | |
| ογ γ | 4 (| gattatetteatgaagttgggtgtaagetggeteatttagetgaggegatteaegt 120 | |
| <u>a</u> . | ~ | TGATCATCTTCATGAAGTTGGTTGTAAATTAGCTCAGCTTGCGGAGGCGATTCACGT | |
| Oy Db | 1204 1286 | tgagittgagtacagaggaittgiggctaacacittagcigaictigaigcitcgaigci 1263 | |
| λο Op | 1264 | tgagottagaccaagtgagattgaatctgttgoggttaactctgtttcgagottcacaa 1323 | |
| 2 | 32 | otottaaasaasetaataaatsaatsaaattettaatataaatsaaattaaaee 138 | |
| . A | 40 | 9 | |
| οy | 1384 | ggagattttcactgtgggttgagcaggaatcgaaccataatagtccgattttcttagatcg 1443 | |

1466 GGTGATTTTCACGGTGGTTGAGCAAGAATCGAACCATAACGGACCGGTTTTCTTAGACCG 1525 δy qq Dp δý g οy q Qγ g οy ολ

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